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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 5 : C12Q 1/68, C07H 21/04	A1	(11) International Publication Number: WO 93/13225 (43) International Publication Date: 8 July 1993 (08.07.93)
(21) International Application Number: PCT/US92/11345 (22) International Filing Date: 21 December 1992 (21.12.92) (30) Priority data: 07/813,585 23 December 1991 (23.12.91) US (71) Applicant: CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). (72) Inventors: KOLBERG, Janice, A. ; 131 Scotts Valley Road, Hercules, CA 94547 (US). URDEA, Michael, S. ; 100 Bunce Meadow Road, Alamo, CA 94507 (US). (74) Agents: KENNEDY, Bill et al.; Morrison & Foerster, 755 Page Mill Road, Palo Alto, CA 94304 (US).		(81) Designated States: CA, JP, KR, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i>
(54) Title: HTLV-1 PROBES FOR USE IN SOLUTION PHASE SANDWICH HYBRIDIZATION ASSAYS (57) Abstract Novel DNA probe sequences for detection of HTLV-1 in a sample in a solution phase sandwich hybridization assay are described. Amplified nucleic acid hybridization assays using the probes are exemplified.		

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5 HTLV-1 PROBES FOR USE IN SOLUTION PHASE
 SANDWICH HYBRIDIZATION ASSAYS

DESCRIPTION

10 Technical Field

 This invention is in the field of nucleic acid hybridization assays. More specifically, it relates to novel nucleic acid probes for detecting HTLV-1.

15 Background Art

 HTLV-1 is a human lymphotropic retrovirus which causes adult T-cell leukemia/lymphoma and tropic spastic paraparesis/HTLV-1-associated myelopathy. These HTLV-1 associated diseases are endemic in Japan and the
20 Caribbean, with sporadic occurrences in the U.S. Detection of HTLV-1 is typically done by immunological or polymerase chain reaction assays (see, e.g., Meytes, et al., Lancet 336(8730):1533-1535, 1990).

 Commonly owned U.S. 4,868,105 describes a
25 solution phase nucleic acid sandwich hybridization assay in which analyte nucleic acid is first hybridized in solution to a labeling probe set and to a capturing probe set in a first vessel. The probe-analyte complex is then transferred to a second vessel that contains a solid-
30 phase-immobilized probe that is substantially complementary to a segment of the capturing probes. The segments hybridize to the immobilized probe, thus removing the complex from solution. Having the analyte in the form of an immobilized complex facilitates
35 subsequent separation steps in the assay. Ultimately,

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single stranded segments of the labeling probe set are hybridized to labeled probes, thus permitting the analyte-containing complex to be detected via a signal generated directly or indirectly from the label.

5 Commonly owned European Patent Application (EPA) 883096976 discloses a variation in the assay described in U.S. 4,868,105 in which the signal generated by the labeled probes is amplified. The amplification involves the use of nucleic acid multimers. These
10 multimers are branched polynucleotides that are constructed to have a segment that hybridizes specifically to the analyte nucleic acid or to a nucleic acid (branched or linear) that is bound to the analyte and iterations of a second segment that hybridize
15 specifically to the labeled probe. In the assay employing the multimer, the initial steps of hybridizing the analyte to label or amplifier probe sets and capturing probe sets in a first vessel and transferring the complex to another vessel containing immobilized
20 nucleic acid that will hybridize to a segment of the capturing probes are followed. The multimer is then hybridized to the immobilized complex and the labeled probes in turn hybridized to the second segment iterations on the multimer. Since the multimers provide
25 a large number of sites for label probe attachment, the signal is amplified. Amplifier and capture probe sequences are disclosed for Hepatitis B virus, Neisseria gonorrhoeae, penicillin and tetracycline resistance in N. gonorrhoeae, and Chlamydia trachomatis.

30 Commonly owned copending application Serial No. 558,897, filed 27 July 1990, describes the preparation of large comb-type branched polynucleotide multimers for use in the above-described solution phase assay. The combs provide greater signal enhancement in the assays than the
35 smaller multimers.

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Disclosure of the Invention

One aspect of the invention is a synthetic oligonucleotide useful as an amplifier probe in a sandwich hybridization assay for HTLV-1 nucleic acid comprising a first segment having a nucleotide sequence substantially complementary to a segment of HTLV-1 nucleic acid, and a second segment having a nucleotide sequence substantially complementary to an oligonucleotide acid multimer.

Another aspect of the invention is a synthetic oligonucleotide useful as a capture probe in a sandwich hybridization assay for HTLV-1 nucleic acid comprising a first segment having a nucleotide sequence substantially complementary to a segment of HTLV-1 nucleic acid; and a second segment having a nucleotide sequence substantially complementary to an oligonucleotide bound to a solid phase.

Another aspect of the invention is a solution sandwich hybridization assay for detecting the presence of HTLV-1 nucleic acid in a sample, comprising

(a) contacting the sample under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence substantially complementary to a segment of HTLV-1 nucleic acid and a second segment having a nucleotide sequence substantially complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence that is substantially complementary to a segment of HTLV-1 nucleic acid and a second segment that is substantially complementary to an oligonucleotide bound to a solid phase;

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(b) contacting the product of step (a) under hybridizing conditions with said oligonucleotide bound to the solid phase;

5 (c) thereafter separating materials not bound to the solid phase;

(d) contacting the product of step (c) under hybridization conditions with the nucleic acid multimer, said multimer comprising at least one oligonucleotide unit that is substantially complementary to the second
10 segment of the amplifier probe polynucleotide and a multiplicity of second oligonucleotide units that are substantially complementary to a labeled oligonucleotide;

(e) removing unbound multimer;

15 (f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;

(g) removing unbound labeled oligonucleotide;
and

20 (h) detecting the presence of label in the solid phase complex product of step (g).

Another aspect of the invention is a kit for the detection of HTLV-1 nucleic acid in a sample comprising in combination

(i) a set of amplifier probe oligonucleotides
25 wherein the amplifier probe oligonucleotide comprises a first segment having a nucleotide sequence substantially complementary to a segment of HTLV-1 nucleic acid and a second segment having a nucleotide sequence substantially complementary to an oligonucleotide unit of a nucleic
30 acid multimer;

(ii) a set of capture probe oligonucleotides wherein the capture probe oligonucleotide comprises a first segment having a nucleotide sequence that is substantially complementary to a segment of HTLV-1
35 nucleic acid and a second segment that is substantially

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complementary to an oligonucleotide bound to a solid phase;

- (iii) a nucleic acid multimer, said multimer comprising at least one oligonucleotide unit that is substantially complementary to the second segment of the amplifier probe polynucleotide and a multiplicity of second oligonucleotide units that are substantially complementary to a labeled oligonucleotide; and
- (iv) a labeled oligonucleotide.

10

Modes for Carrying Out the Invention

Definitions

- "Solution phase nucleic acid hybridization assay" intends the assay techniques described and claimed in commonly owned U.S. Patent No. 4,868,105 and EPA 883096976.

- A "modified nucleotide" intends a nucleotide monomer that may be stably incorporated into a polynucleotide and which has an additional functional group. Preferably, the modified nucleotide is a 5'-cytidine in which the N⁴-position is modified to provide a functional hydroxy group.

- An "amplifier multimer" intends a branched polynucleotide that is capable of hybridizing simultaneously directly or indirectly to analyte nucleic acid and to a multiplicity of polynucleotide iterations (i.e., either iterations of another multimer or iterations of a labeled probe). The branching in the multimers is effected through covalent bonds and the multimers are composed of two types of oligonucleotide units that are capable of hybridizing, respectively, to analyte nucleic acid or nucleic acid hybridized to analyte nucleic acid and to a multiplicity of labeled probes. The composition and preparation of such

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multimers are described in EPA 883096976 and U.S. Serial No. 558,897 filed 27 July 1990, the disclosures of which are incorporated herein by reference.

5 The term "amplifier probe" is intended as a branched or linear polynucleotide that is constructed to have a segment that hybridizes specifically to the analyte nucleic acid and iterations of a second segment that hybridize specifically to an amplifier multimer.

10 The term "capture probe" is intended as an oligonucleotide having a segment substantially complementary to a nucleotide sequence of the target DNA and a segment that is substantially complementary to a nucleotide sequence of a solid-phase-immobilized probe.

15 "Large" as used herein to describe the comb-type branched polynucleotides of the invention intends a molecule having at least about 15 branch sites and at least about 20 iterations of the labeled probe binding sequence.

20 "Comb-type" as used herein to describe the structure of the branched polynucleotides of the invention intends a polynucleotide having a linear backbone with a multiplicity of sidechains extending from the backbone.

25 A "cleavable linker molecule" intends a molecule that may be stably incorporated into a polynucleotide chain and which includes a covalent bond that may be broken or cleaved by chemical treatment or physical treatment such as by irradiation.

30 All nucleic acid sequences disclosed herein are written in a 5' to 3' direction. Nucleotides are designated according to the nucleotide symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. All nucleotide sequences disclosed are intended to include complementary sequences unless
35 otherwise indicated.

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Solution Phase Hybridization Assay

The general protocol for the solution phase sandwich hybridizations is as follows. The analyte nucleic acid is placed in a microtiter well with an excess of two single-stranded nucleic acid probe sets:

5 (1) a set of capture probes, each having a first binding sequence substantially complementary to the analyte and a second binding sequence that is substantially complementary to nucleic acid bound to a solid support,

10 for example, the well surface or a bead, and (2) a set of amplifier probes (branched or linear), each having a first binding sequence that is capable of specific binding to the analyte and a second binding sequence that is capable of specific binding to a segment of the

15 multimer. The resulting product is a three component nucleic acid complex of the two probes hybridized to the analyte by their first binding sequences. The second binding sequences of the probes remain as single-stranded segments as they are not complementary to the analyte.

20 This complex hybridizes to the immobilized probe on the solid surface via the second binding sequence of the capture probe. The resulting product comprises the complex bound to the solid surface via the duplex formed by the oligonucleotide bound to the solid surface and the

25 second binding sequence of the capture probe. Unbound materials are then removed from the surface such as by washing.

The amplification multimer is then added to the bound complex under hybridization conditions to permit

30 the multimer to hybridize to the available second binding sequence(s) of the amplifier probe of the complex. The resulting complex is then separated from any unbound multimer by washing. The labeled oligonucleotide is then added under conditions which permit it to hybridize to

35 the substantially complementary oligonucleotide units of

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the multimer. The resulting immobilized labeled nucleic acid complex is then washed to remove unbound labeled oligonucleotide, and read.

The analyte nucleic acids may be from a variety of sources, e.g., biological fluids or solids, and may be prepared for the hybridization analysis by a variety of means, e.g., proteinase K/SDS, chaotropic salts, etc. Also, it may be of advantage to decrease the average size of the analyte nucleic acids by enzymatic, physical or chemical means, e.g., restriction enzymes, sonication, chemical degradation (e.g., metal ions), etc. The fragments may be as small as 0.1 kb, usually being at least about 0.5 kb and may be 1 kb or higher. The analyte sequence is provided in single-stranded form for analysis. Where the sequence is naturally present in single-stranded form, denaturation will not be required. However, where the sequence may be present in double-stranded form, the sequence should be denatured. Denaturation can be carried out by various techniques, such as alkali, generally from about 0.05 to 0.2 M hydroxide, formamide, salts, heat, enzymes, or combinations thereof.

The first binding sequences of the capture probe and amplifier probe that are substantially complementary to the analyte sequence will each be of at least 15 nucleotides, usually at least 25 nucleotides, and not more than about 5 kb, usually not more than about 1 kb, preferably not more than about 100 nucleotides. They will typically be approximately 30 nucleotides. They will normally be chosen to bind to different sequences of the analyte. The first binding sequences may be selected based on a variety of considerations. Depending upon the nature of the analyte, one may be interested in a consensus sequence, a sequence associated

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with polymorphisms, a particular phenotype or genotype, a particular strain, or the like.

The number of different amplifier and capture probes used influences the sensitivity of the assay, because the more probe sequences used, the greater the signal provided by the assay system. Furthermore, the use of more probe sequences allows the use of more stringent hybridization conditions, thereby reducing the incidence of false positive results. Thus, the number of probes in a set will be at least one capture probe and at least one amplifier probe, more preferably two capture and two amplifier probes, and most preferably 5-100 capture probes and 5-100 amplifier probes.

Oligonucleotide probes for HTLV-1 were designed by aligning the nucleotide sequences of the pol gene of HTLV-1 Japanese and Caribbean isolates and HTLV-2 available from GenBank. Regions of greatest homology between HTLV-1 isolates were chosen for capture probes, while regions of lesser homology were chosen as amplifier probes. Thus, as additional strains or isolates of HTLV-1 are made available, appropriate probes made be designed by aligning the sequence of the new strain or isolate with the nucleotide sequences used to design the probes of the present invention, and choosing regions of greatest homology for use as capture probes, with regions of lesser homology chosen as amplifier probes. The capture probes of the presently preferred configuration form two clusters, with the amplifier probes clustered between the two capture probe clusters. The nucleotide sequences of the presently preferred probe sets are shown in the examples.

The second binding sequences of the capture probe and amplifier probe are selected to be substantially complementary, respectively, to the oligonucleotide bound to the solid surface and to a

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segment of the multimer and so as to not be encountered by endogenous sequences in the sample/analyte. The second binding sequence may be contiguous to the first binding sequence or be spaced therefrom by an
5 intermediate noncomplementary sequence. The probes may include other noncomplementary sequences if desired. These noncomplementary sequences must not hinder the binding of the binding sequences or cause nonspecific binding to occur.

10 The capture probe and amplifier probe may be prepared by oligonucleotide synthesis procedures or by cloning, preferably the former.

It will be appreciated that the binding sequences need not have perfect complementarity to
15 provide homoduplexes. In many situations, heteroduplexes will suffice where fewer than about 10% of the bases are mismatches, ignoring loops of five or more nucleotides. Accordingly, as used herein the term "complementary" intends exact complementarity wherein each base within
20 the binding region corresponds exactly, and "substantially complementary" intends 90% or greater homology.

The labeled oligonucleotide will include a sequence substantially complementary to the repeated
25 oligonucleotide units of the multimer. The labeled oligonucleotide will include one or more molecules ("labels"), which directly or indirectly provide a detectable signal. The labels may be bound to individual members of the substantially complementary sequence or
30 may be present as a terminal member or terminal tail having a plurality of labels. Various means for providing labels bound to the oligonucleotide sequences have been reported in the literature. See, for example, Leary et al., Proc. Natl. Acad. Sci. USA (1983) 80:4045;
35 Renz and Kurz, Nucl. Acids Res. (1984) 12:3435;

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Richardson and Gumpert, Nucl. Acids Res. (1983) 11:6167; Smith et al., Nucl. Acids. Res. (1985) 13:2399; Meinkoth and Wahl, Anal. Biochem. (1984) 138:267. The labels may be bound either covalently or non-covalently to the

5 substantially complementary sequence. Labels which may be employed include radionuclides, fluorescers, chemiluminescers, dyes, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, enzyme subunits, metal ions, and the like. Illustrative specific labels

10 include fluorescein, rhodamine, Texas red, phycoerythrin, umbelliferone, luminol, NADPH, α - β -galactosidase, horse-radish peroxidase, alkaline phosphatase, etc.

The ratio of capture probe and amplifier probe to anticipated moles of analyte will each be at least

15 stoichiometric and preferably in excess. This ratio is preferably at least about 1.5:1, and more preferably at least 2:1. It will normally be in the range of 2:1 to 10^6 :1. Concentrations of each of the probes will generally range from about 10^{-5} to 10^{-9} M, with sample nucleic

20 acid concentrations varying from 10^{-21} to 10^{-12} M. The hybridization steps of the assay will generally take from about 10 minutes to 20 hours, frequently being completed in about 1 hour. Hybridization can be carried out at a mildly elevated temperature, generally in the range from

25 about 20°C to 80°C, more usually from about 35°C to 70°C, particularly 65°C.

The hybridization reactions are usually done in an aqueous medium, particularly a buffered aqueous medium, which may include various additives. Additives

30 which may be employed include low concentrations of detergent (0.01 to 1%), salts, e.g., sodium citrate (0.017 to 0.17 M), Ficoll, polyvinylpyrrolidone, carrier nucleic acids, carrier proteins, etc. Nonaqueous solvents may be added to the aqueous medium, such as

35 dimethylformamide, dimethylsulfoxide, alcohols, and

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formamide. These other solvents are generally present in amounts ranging from 2 to 50%.

The stringency of the hybridization medium may be controlled by temperature, salt concentration, solvent system, and the like. Thus, depending upon the length and nature of the sequence of interest, the stringency will be varied.

Depending upon the nature of the label, various techniques can be employed for detecting the presence of the label. For fluorescers, a large number of different fluorometers are available. For chemiluminescers, luminometers or films are available. With enzymes, a fluorescent, chemiluminescent, or colored product can be provided and determined fluorometrically, luminometrically, spectrophotometrically or visually. The various labels which have been employed in immunoassays and the techniques applicable to immunoassays can be employed with the subject assays.

Kits for carrying out amplified nucleic acid hybridization assays according to the invention will comprise in packaged combination the following reagents: the amplifier probe or set of probes; the capture probe or set of probes; the amplifier multimer; and an appropriate labeled oligonucleotide. These reagents will typically be in separate containers in the kit. The kit may also include a denaturation reagent for denaturing the analyte, hybridization buffers, wash solutions, enzyme substrates, negative and positive controls and written instructions for carrying out the assay.

The following examples further illustrate the invention. These examples are not intended to limit the invention in any manner.

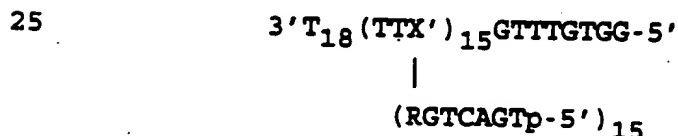
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EXAMPLESExample ISynthesis of Comb-type Branched Polynucleotide

5 This example illustrates the synthesis of a comb-type branched polynucleotide having 15 branch sites and sidechain extensions having three labeled probe binding sites. This polynucleotide was designed to be used in a solution phase hybridization as described in EPA 883096976.

10 All chemical syntheses of oligonucleotides were performed on an automatic DNA synthesizer (Applied Biosystems, Inc., (ABI) model 380 B). Phosphoramidite chemistry of the beta cyanoethyl type was used including 5'-phosphorylation which employed Phostel™ reagent (ABN).
 15 Standard ABI protocols were used except as indicated. Where it is indicated that a multiple of a cycle was used (e.g., 1.2 cycle), the multiple of the standard amount of amidite recommended by ABI was employed in the specified cycle. Appended hereto are the programs for carrying out
 20 cycles 1.2 and 6.4 as run on the Applied Biosystems Model 380 B DNA Synthesizer.

A comb body of the following structure was first prepared:



wherein X' is a branching monomer, and R is a periodate cleavable linker.

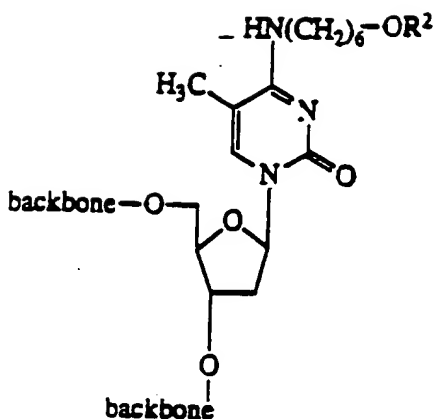
30 The portion of the comb body through the 15 (TTX') repeats is first synthesized using 33.8 mg aminopropyl-derivatized thymidine controlled pore glass (CPG) (2000 Å, 7.4 micromoles thymidine per gram support) with a 1.2 cycle protocol. The branching site
 35 nucleotide was of the formula:

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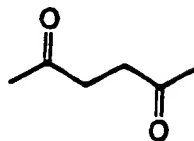
5

10

15



20

where R^2 represents

25

For synthesis of the comb body (not including sidechains), the concentration of beta cyanoethylphosphoramidite monomers was 0.1 M for A, C, G and T, 0.15 M for the branching site monomer E, and 0.2 M for Phostel™ reagent. Detritylation was done with 3% trichloroacetic acid in methylene chloride using stepped flowthrough for the duration of the deprotection. At the conclusion the 5' DMT was replaced with an acetyl group.

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Cleavable linker R and six base sidechain extensions of the formula 3'-RGTCAGTp (SEQ ID NO:1) were synthesized at each branching monomer site as follows. The base protecting group removal (R^2 in the formula above) was performed manually while retaining the CPG support in the same column used for synthesizing the comb body. In the case of R^2 = levuliny1, a solution of 0.5 M hydrazine hydrate in pyridine/glacial acetic acid (1:1 v/v) was introduced and kept in contact with the CPG support for 90 min with renewal of the liquid every 15 min, followed by extensive washing with pyridine/glacial acetic acid (1:1 v/v) and then by acetonitrile. After the deprotection the cleavable linker R and six base sidechain extensions were added using a 6.4 cycle.

In these syntheses the concentration of phosphoramidites was 0.1 M (except 0.2 M R and Phostel™ reagent; R was 2-(4-(4-(2-Dimethoxytrityloxy)ethyl)-phenoxy 2,3-di(benzoyloxy)-butyloxy)phenyl)ethyl-2-cyanoethyl-N,N-diisopropylphosphoramidite).

Detritylation is effected with a solution of 3% trichloroacetic acid in methylene chloride using continuous flowthrough, followed by a rinse solution of toluene/chloromethane (1:1 v/v). Branched polynucleotide chains were removed from the solid supports automatically in the 380B using the cycle "CE NH_3 ." The ammonium hydroxide solution was collected in 4 ml screw-capped Wheaton vials and heated at 60°C for 12 hr to remove all base-protecting groups. After cooling to room temperature the solvent was removed in a Speed-Vac evaporator and the residue dissolved in 100 μ l water.

3' backbone extensions (segment A), sidechain extensions and ligation template/linkers of the following structures were also made using the automatic synthesizer:

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3' Backbone

extension 3'-TCCGTATCCTGGGCACAGAGGTGCP-5' (SEQ ID NO:2)

Sidechain

extension 3'-GATGCG(TTCATGCTGTTGGTGTAG)₃-5' (SEQ ID NO:3)

5 Ligation
template for
linking 3'
backbone
extension

3'-AAAAAAAAAAGCACCTp-5' (SEQ ID NO:4)

10 Ligation tem-
plate for link-
ing sidechain
extension

3'-CGCATCACTGAC-5' (SEQ ID NO:5)

15 The crude comb body was purified by a standard
polyacrylamide gel (7% with 7 M urea and 1X TBE running
buffer) method.

The 3' backbone extension and the sidechain
extensions were ligated to the comb body as follows. The
comb body (4 pmole/ μ l), 3' backbone extension (6.25
pmole/ μ l), sidechain extension (93.75 pmole/ μ l),
20 sidechain linking template (75 pmoles/ μ l) and backbone
linking template (5 pmole/ μ l) were combined in 1 mM ATP/
5 mM DTT/ 50 mM Tris-HCl, pH 8.0/ 10 mM MgCl₂/ 2 mM
spermidine, with 0.5 units/ μ l T4 polynucleotide kinase.
The mixture was incubated at 37°C for 2 hr, then heated
25 in a water bath to 95°C, and then slowly cooled to below
35°C over a 1 hr period. 2 mM ATP, 10 mM DTT, 14%
polyethylene glycol, and 0.21 units/ μ l T4 ligase were
added, and the mixture incubated for 16-24 hr at 23°C.
The DNA was precipitated in NaCl/ethanol, resuspended in
30 water, and subjected to a second ligation as follows.
The mixture was adjusted to 1 mM ATP, 5 mM DTT, 14%
polyethylene glycol, 50 mM Tris-HCl, pH 7.5, 10 mM MgCl₂,
2 mM spermidine, 0.5 units/ μ l T4 polynucleotide kinase,
and 0.21 units/ μ l T4 ligase were added, and the mixture

35

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incubated at 23°C for 16-24 hr. Ligation products were then purified by polyacrylamide gel electrophoresis.

After ligation and purification, a portion of the product was labeled with ^{32}P and subjected to cleavage at the site of R achieved by oxidation with aqueous NaIO_4 for 1 hr. The sample was then analyzed by PAGE to determine the number of sidechain extensions incorporated by quantitating the radioactive label in the bands on the gel. The product was found to have a total of 45 labeled probe binding sites.

Example II

Procedure for HTLV-1 Assay

A "15 X 3" amplified solution phase nucleic acid sandwich hybridization assay format is used in this assay. The "15 x 3" designation derives from the fact that the format employs two multimers: (1) an amplifier probe having a first segment (A) that binds to HTLV-1 and a second segment (B) that hybridizes to (2) an amplifier multimer having a first segment (B*) that hybridizes to the segment (B) and fifteen iterations of a segment (C), wherein segment C hybridizes to three labeled oligonucleotides.

The amplifier and capture probe segments and their respective names used in this assay are as follows.

HTLV-1 Amplifier Probes

HTLV.7 (SEQ ID NO:6)
GGTCTGGGTGTCAAYCTGGGCTTTAATTACGGG
HTLV.8 (SEQ ID NO:7)
ATCTAGTARAGCTTCGATAGTCTTTGGGTGGCT
HTLV.9 (SEQ ID NO:8)
GGCTATCGGAAGGACTGTCATGTCGCTCCTGT
HTLV.10 (SEQ ID NO:9)
TGTRTTTTTGAGGGGAGTATTACTTGAGAACAA

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HTLV.11 (SEQ ID NO:10)
ATCTTGGGTTTGGCCCCCTGCCCTAAYACGGA
HTLV.12 (SEQ ID NO:11)
TATTAGCACAGGAAGGGAGGTGAGCTTAAAGTG
5 HTLV.13 (SEQ ID NO:12)
TAAACAATAGGCGTYGTCCGAAAGGGAGGCG
HTLV.14 (SEQ ID NO:13)
CYAGTTGTTTTTGGTATCAACTAGGCAAGATGT
HTLV.15 (SEQ ID NO:14)
10 GCATTGTTGTAAGGCATCRGACCTATGATGGC
HTLV.16 (SEQ ID NO:15)
CCYTTTTTGCCTCAGGGAGGTACAGGACGCCYTG
HTLV.17 (SEQ ID NO:16)
RGCTGGCGCCTGTATTGGCAAGATTACAGGCGG
15 HTLV.18 (SEQ ID NO:17)
GGGGGGCCTTGGGAGGTGTTCTAGYCCAAGGAC
HTLV.19 (SEQ ID NO:18)
GGCGTTCGTTTAAAGGGAAGTGGCTGATTTG
HTLV.20 (SEQ ID NO:19)
20 GGGCCITCCGGACCAAGTGTGCAAGGCCTGGA
HTLV.21 (SEQ ID NO:20)
GCCCCGTGTAGGRTTCGATATGGCCTGCCTCCA
HTLV.22 (SEQ ID NO:21)
CYTTTTTAAGTGGGAATACTGGGTTATTTCCTG
25 HTLV.23 (SEQ ID NO:22)
GCAGGTCGTGGATGAATGCCAGGTTCCATTGG
HTLV.24 (SEQ ID NO:23)
ATGAGAGRTCTATGGTTAGAGAGTTAGTGGCCC
HTLV.25 (SEQ ID NO:24)
30 GGCTGGACAAGTCAGGGGGCCCCGGGGGAAGATG
HTLV.26 (SEQ ID NO:25)
CTATAGTTTGYAAGTGGGCTAGTGTRGTTGGCA
HTLV.27 (SEQ ID NO:26)
GTARGGGGATTGGAAAAAGGCGTCTYTAAGGT
35 HTLV.28 (SEQ ID NO:27)

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CAGTGAAAGCAAAGTAGGGCTGGAAGTGTGTTAG
HTLV.29 (SEQ ID NO:28)
TAGTGCCGGGGCCGTAGTTACACTGCTGTGGGA
HTLV.30 (SEQ ID NO:29)
5 TAAACCCTTGGGGTAGTACTYTCAGGCGTATC
HTLV.31 (SEQ ID NO:30)
CCAGCTGCATTTTGAACAGGGTGGGACTATTTT
HTLV.32 (SEQ ID NO:31)
GGAARGCTTGCCGAATGGGCTGCAGGATATGGG
10 HTLV.33 (SEQ ID NO:32)
TGTCATCCATGTACTGAAGAATAGTGCATTGGG
HTLV.34 (SEQ ID NO:33)
GYAGGTCCCKCATGGGAGGGGCTTGCTYAGGAGAA
HTLV.35 (SEQ ID NO:34)
15 TTAGGGAAGCCATTGTGGCCTCTGAGAGTAGTW
HTLV.36 (SEQ ID NO:35)
TTTTGTTTTTCGGACACAGGCAACCCATGGGAGA
HTLV.37 (SEQ ID NO:36)
CTAGGAACTTAATTGTTCCAGGGGTTTGCTGGG
20 HTLV.38 (SEQ ID NO:37)
CATAAGTGAGGTGATTRGGTGAAATTATYTGCC
HTLV.39 (SEQ ID NO:38)
AGCGGGACCGTATAGGTACCKTGGGGACTGCAT
HTLV.40 (SEQ ID NO:39)
25 CGCCAAGTAGGGCTTGAAGTTCAGGTAGCGCCC
HTLV.41 (SEQ ID NO:40)
AGGTAGGAGTTCCTTTGGAGACCCACTGAATCT
HTLV.42 (SEQ ID NO:41)
AGGCACAGTAGAGACTGTGAAGGGGCTGGCGTA
30

HTLV-1 Capture Probes

HTLV.1 (SEQ ID NO:42)
TCTGGTTCGCGGATAGTGGGCTTTAGGCGGGG
HTLV.2 (SEQ ID NO:43)
35 GGGAGRTCTAATAGGAGGGCATCYTCCTCTGGC

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HTLV.3 (SEQ ID NO:44)
CCTATGRAGTTTTTTGGGTGTGGRATGTCRGCG
HTLV.4 (SEQ ID NO:45)
CTGTAATGTGGGGGGGAGGTTAAACCTCCCCC
5 HTLV.5 (SEQ ID NO:46)
AATAGATGYTGCGTCTTGTTARGAARGACTTG
HTLV.6 (SEQ ID NO:47)
CCGACGGGCGGGATCTAACGGTATAACTGGCAG
HTLV.43 (SEQ ID NO:48)
10 ATATTTGGTCTCGGGGATCAGTATGCCTTTGTA
HTLV.44 (SEQ ID NO:49)
GCACTAATGATTGAACTTGAGAAGGATTTAAAT
HTLV.45 (SEQ ID NO:50)
TGCGGCAGTTCTGTGACAGGGCCTGCCGCAGCT
15 HTLV.46 (SEQ ID NO:51)
CCCCTAGGAGGGGCAGGGTTTGGACTAGTCTAC
HTLV.47 (SEQ ID NO:52)
CAGTRGTGGTGCCAGTGAGGGTCAGCATAATAG
HTLV.48 (SEQ ID NO:53)
20 CAAGTGGCCACTGCTSCTTGGACTGGAACACYA

Each amplifier probe contains, in addition to the sequences substantially complementary to the HTLV-1 sequences, the following 5' extension complementary to a segment of the amplifier multimer,

25 AGGCATAGGACCCGTGTCTT (SEQ ID NO:54).

Each capture probe contains, in addition to the sequences substantially complementary to HTLV-1 DNA, the following downstream sequence complementary to DNA bound to the solid phase (XT1*),

30 CTTCCTTGGAGAAAGTGGTG (SEQ ID NO:55).

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Microtiter plates were prepared as follows. White Microlite 1 Removawell strips (polystyrene microtiter plates, 96 wells/plate) were purchased from Dynatech Inc. Each well was filled with 200 μ l 1 N HCl and incubated at room temperature for 15-20 min. The plates were then washed 4 times with 1X PBS and the wells aspirated to remove liquid. The wells were then filled with 200 μ l 1 N NaOH and incubated at room temperature for 15-20 min. The plates were again washed 4 times with 1X PBS and the wells aspirated to remove liquid.

Poly(phe-lys) was purchased from Sigma Chemicals, Inc. This polypeptide has a 1:1 molar ratio of phe:lys and an average m.w. of 47,900 gm/mole. It has an average length of 309 amino acids and contains 155 amines/mole. A 1 mg/ml solution of the polypeptide was mixed with 2M NaCl/1X PBS to a final concentration of 0.1 mg/ml (pH 6.0). 100 μ L of this solution was added to each well. The plate was wrapped in plastic to prevent drying and incubated at 30°C overnight. The plate was then washed 4 times with 1X PBS and the wells aspirated to remove liquid.

The following procedure was used to couple the oligonucleotide XT1* to the plates. Synthesis of XT1* was described in EPA 883096976. 20 mg disuccinimidyl suberate was dissolved in 300 μ l dimethyl formamide (DMF). 26 OD₂₆₀ units of XT1* was added to 100 μ l coupling buffer (50 mM sodium phosphate, pH 7.8). The coupling mixture was then added to the DSS-DMF solution and stirred with a magnetic stirrer for 30 min. An NAP-25 column was equilibrated with 10 mM sodium phosphate, pH 6.5. The coupling mixture DSS-DMF solution was added to 2 ml 10 mM sodium phosphate, pH 6.5, at 4°C. The mixture was vortexed to mix and loaded onto the equilibrated NAP-25 column. DSS-activated XT1* DNA was eluted from the column with 3.5 ml 10 mM sodium

-22-

phosphate, pH 6.5. 5.6 OD₂₆₀ units of eluted DSS-activated XT1* DNA was added to 1500 ml 50 mM sodium phosphate, pH 7.8. 50 µl of this solution was added to each well and the plates were incubated overnight. The plate was then washed 4 times with 1X PBS and the wells aspirated to remove liquid.

Final stripping of plates was accomplished as follows. 200 µL of 0.2N NaOH containing 0.5% (w/v) SDS was added to each well. The plate was wrapped in plastic and incubated at 65°C for 60 min. The plate was then washed 4 times with 1X PBS and the wells aspirated to remove liquid. The stripped plate was stored with desiccant beads at 2-8°C.

Test samples were prepared as follows. 1 X 10⁶ HTLV-1-infected MT-2 cells or uninfected HuT cells (Human T cell lymphoma cells) were used directly in the assay below or were extracted with a standard phenol:chloroform extraction procedure (See, for example, Sambrook, et al., Molecular Cloning: A Laboratory Manual, 1989, Cold Spring Harbor Press, Cold Spring Harbor, NY). Negative controls were Dulbecco's Modified Eagle's Medium (DMEM), negative human serum (neg. HS), buffer (10 mM Tris-HCl, pH 8.0), and distilled H₂O. 60 µl P-K Buffer (2 mg/ml proteinase K in 10 mM Tris-HCl, pH 8.0/0.15 M NaCl/10 mM EDTA, pH 8.0/1% SDS/40µg/ml sonicated salmon sperm DNA) was added to a microfuge tube for each sample to be assayed. 50 µl of test sample was added to each tube.

A cocktail of the HTLV-1-specific amplifier and capture probes listed above was added to each well (10 fmoles of each probe/tube in 25 µl, diluted in 1 N NaOH). The tubes were incubated at 65°C for 30 min.

65 µl neutralization buffer was then added to each tube (0.77 M 3-(N-morpholino)propane sulfonic acid/1.845 M NaCl/0.185 M sodium citrate). After mixing, the tubes were incubated at 65°C overnight. Condensation

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was centrifuged off the walls of each tube and the contents of the tubes transferred to microtiter wells prepared as above. The microtiter plates were incubated at 65°C for 4 hr.

5 After an additional 10 min at room temperature, the contents of each well are aspirated to remove all fluid, and the wells washed 2X with washing buffer (0.1% SDS/0.015 M NaCl/ 0.0015 M sodium citrate).

10 The amplifier multimer is then added to each well (20 fmoles in 50 μ l in 50% horse serum/(0.06 M NaCl/0.06 M sodium citrate/0.1% SDS mixed 1:1 with 4X SSC/0.1% SDS/.5% "blocking reagent" (Boehringer Mannheim, catalog No. 1096 176). After covering plates and
15 agitating to mix the contents in the wells, the plates are incubated for 30 min at 55°C. After a further 5 min period at room temperature, the wells are washed as described above.

Alkaline phosphatase label probe, disclosed in EP 883096976, is then added to each well (20 fmoles in 50
20 μ l/well). After incubation at 55°C for 15 min, and 5 min at room temperature, the wells are washed twice as above and then 3X with 0.015 M NaCl/0.0015 M sodium citrate.

An enzyme-triggered dioxetane (Schaap et al., Tet. Lett. (1987) 28:1159-1162 and EPA Pub. No. 0254051),
25 obtained from Lumigen, Inc., was employed. 50 μ l Lumiphos 530 (Lumigen) was added to each well. The wells were tapped lightly so that the reagent would fall to the bottom and gently swirled to distribute the reagent evenly over the bottom. The wells were covered and
30 incubated at 37°C for 40 min.

Plates are then read on a Dynatech ML 1000 luminometer. Output is given as the full integral of the light produced during the reaction.

Results are shown in the Table below. These
35 results indicate the ability to detect HTLV-1 DNA in both

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extracted and unextracted infected cells, and no cross-hybridization with components of the uninfected controls.

Table

5	Sample	# Cells	Sample Prep	Luminometer Reading
	MT-2	10 ⁶	extracted	48.68
	HuT 78	10 ⁶	extracted	1.91
	MT-2	10 ⁶	unextracted	27.39
10	HuT-78	10 ⁶	unextracted	2.37
	DMEM	0	unextracted	1.75
	Neg. HS	0	unextracted	1.07
	Tris	0	unextracted	1.39
	H ₂ O	0	unextracted	1.02

15

Example 3Detection of HTLV-1 RNA

HTLV-1 RNA is detected using essentially the same procedure as above with the following modifications.

20 A standard curve of HTLV-1 RNA is prepared by serially diluting HTLV-1 virus stock in normal human serum to a range between 125 to 5000 TCID₅₀/ml. A proteinase K solution is prepared by adding 10 mg proteinase K to 5 ml HTLV-1 capture diluent (53 mM Tris-HCl, pH 8/ 10.6 mM EDTA/ 1.3% SDS/ 16 µg/ml sonicated salmon sperm DNA/ 5.3X SSC/ 1 mg/ml proteinase K) made 7% in formamide stored at -20°C. Equimolar mixtures of capture probes and label probes are added to the proteinase K solution such that the final concentration of each probe was 1670 fmoles/ml. After addition of 30 µl of the probe/proteinase K solution to each well of microtiter plates prepared as above, 10 µl of appropriate virus dilutions are added to each well. Plates are covered, shaken to mix and then incubated at 65°C for 16 hr.

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Plates are removed from the incubator and cooled on the bench top for 10 min. The wells are washed 2X as described in Example 2 above. The 15 X 3 multimer is diluted to 1 fmole/ μ l in Amp/Label diluent (prepared by mixing 2.22 ml DEPC-treated H₂O (DEPC is diethylpyrocarbonate), 1.35 ml 10% SDS, 240 μ l 1 M Tris pH 8.0, 20 μ l horse serum, adjusted to 2 mg/ml in proteinase K and heated to 65°C for 2 hr, then added to 240 μ l of 0.1 M PMSF and heated at 37°C for 1 hr, after which is added 4 ml DEPC-H₂O, 4 ml 10 % SDS and 8 ml 20X SSC). The diluted 15 X 3 multimer is added at 40 μ l/well, the plates sealed, shaken, and incubated at 55°C for 30 min.

The plates are then cooled at room temperature for 10 minutes, and washed as described above. Alkaline phosphatase label probe is diluted to 2.5 fmoles/ μ l in Amp/Label diluent and 40 μ l added to each well. Plates are covered, shaken, and incubated at 55°C for 15 min.

Plates are cooled 10 min at room temperature, washed 2X as above and then 3X with 0.15 M NaCl/0.015 M sodium citrate. Substrate is added and luminescence measured as above.

Modifications of the above-described modes for carrying out the invention that are obvious to those of skill in biochemistry, nucleic acid hybridization, and related fields are intended to be within the scope of the following claims.

30

35

-26-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Kolberg, Janice A.
Urdea, Michael S.
- (ii) TITLE OF INVENTION: HTLV-1 PROBES FOR USE IN SOLUTION
PHASE SANDWICH HYBRIDIZATION ASSAYS
- (iii) NUMBER OF SEQUENCES: 55
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Morrison & Foerster
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- 15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 20 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 07/813,585
(B) FILING DATE: 18-DEC-1991
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Thomas E. Ciotti
(B) REGISTRATION NUMBER: 21,013
(C) REFERENCE/DOCKET NUMBER: 22300-20238.00
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(A) TELEPHONE: 415-813-5600
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(C) TELEX: 706141

30 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTGR

7

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGTGGAGACA CGGGTCCTAT GCCT

24

(2) INFORMATION FOR SEQ ID NO:3:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATGTGGTTG TCGTACTTGA TGTGGTTGTC GTACTTGATG TGGTTGTCGT ACTTGCGTAG

60

(2) INFORMATION FOR SEQ ID NO:4:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 TCCACGAAAA AAAAAA

16

(2) INFORMATION FOR SEQ ID NO:5:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGTCACTAC GC

12

5 (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTCTGGGTG TCAAYCTGGG CTTRAATTAC GGG

33

(2) INFORMATION FOR SEQ ID NO:7:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCTAGTARA GCTTCGATAG TCTTTGGGTG GCT

33

(2) INFORMATION FOR SEQ ID NO:8:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCTATCGGA AGGACTGTCA TGTCTGCTCC TGT

33

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid

35

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5

TGTRTTTTTG AGGGGAGTAT TACTTGAGAA CAA

33

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15

ATCTTGGGTT TGGCCCCCTG CCCCTAAYAC GGA

33

(2) INFORMATION FOR SEQ ID NO:11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25

TATTAGCACA GGAAGGGAGG TGAGCTTAAA GTG

33

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35

TAAACAATA GCGTYGTCC GGAAAGGGAG GCG

33

(2) INFORMATION FOR SEQ ID NO:13:

-30-

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CYAGTTGTTT TTGGTATCAA CTAGGCAAGA TGT

33

(2) INFORMATION FOR SEQ ID NO:14:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCATTGTGT AAGGCATCRC GACCTATGAT GGC

33

(2) INFORMATION FOR SEQ ID NO:15:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCYTTTTGCC TCAGGGAGGT ACAGGACGCC YTG

33

(2) INFORMATION FOR SEQ ID NO:16:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

35 RGCTGGCGCC TGTATTGGCA AGATTACAGG CGG

33

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGCCTT GGGAGGTGTT CTAGYCCAAG GAC

33

10 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCGTTCTGG TTAAAGGGA ACTGGCTGAT TTS

33

20 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGCCTTCCG GACCAAGTGT TGCAAGGCCT GGA

33

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

-32-

GCCCCGGTGTA GGRITCGATA TGGCCTGCCT CCA

33

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10 CYTTTTTAAC TGGGAATACT GGGTTATTYC CTG

33

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20 GCAGGTCGTG GATGAATCGC CAGGTCCAT TGG

33

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30 ATGAGAGRTC TATGGTTAGA GAGTTAGTGG CCC

33

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

-33-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTGGACAA GTCAGGGGGC CCGGGGAAG ATG

33

(2) INFORMATION FOR SEQ ID NO:25:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTATAGTTTG YAAGTGGGCT AGTGTRGTTG GCA

33

(2) INFORMATION FOR SEQ ID NO:26:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTARGGGGAT TTGGAAAAG GCGTCTYTAA GGT

33

(2) INFORMATION FOR SEQ ID NO:27:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

30 CAGTGAAAGC AAAGTAGGGC TGGAACTGTT TAG

33

(2) INFORMATION FOR SEQ ID NO:28:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-34-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGTGCCGGG GCCGTAGTTA CACTGCTGTG GGA

33

5 (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAACCCCTTG GGGTAGTACT YTCCAGGCGT ATC

33

(2) INFORMATION FOR SEQ ID NO:30:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAGCTGCAT TTCGAACAGG GTGGGACTAT TTT

33

(2) INFORMATION FOR SEQ ID NO:31:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGAARGCTTG CCGAATGGGC TGCAGGATAT GGG

33

(2) INFORMATION FOR SEQ ID NO:32:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid

-35-

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGTCATCCAT GTACTGAAGA ATAGTGCAAT GGG

33

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

15 GYAGGTCKC ATGGGAGGGG CTTGCTAGGA GAA

33

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTAGGGAAGC CATTGTGGCC TCTGAGAGTA GTW

33

25 (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTTGTTTTT GGACACAGGC AACCCATGGG AGA

33

(2) INFORMATION FOR SEQ ID NO:36:

35

-36-

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTAGGAACCTT AATTGTTCCA GGGGTTTGCT GGG

33

(2) INFORMATION FOR SEQ ID NO:37:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CATAAGTGAG GTGATTGGT GAAATTATYT GCC

33

(2) INFORMATION FOR SEQ ID NO:38:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCGGGACCG TATAGGTACC KTGGGGACTG CAT

33

(2) INFORMATION FOR SEQ ID NO:39:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGCCAAGTAG GGCTTGAAGT TCAGGTAGCG CCC

33

-37-

(2) INFORMATION FOR SEQ ID NO:40:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGGTAGGAGT TCCTTTGGAG ACCCACTGAA TCT

33

10 (2) INFORMATION FOR SEQ ID NO:41:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGGCACAGTA GAGACTGTGA AGGGGCTGGC GTA

33

20 (2) INFORMATION FOR SEQ ID NO:42:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTGGTTCTG GGATAGTGGG CTTTAGGCCG GGG

33

(2) INFORMATION FOR SEQ ID NO:43:

- 30 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

-38-

GGGAGRTCTA ATAGGAGGGC ATCYTCCTCT GGC

33

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

10 CCTATGRAGT TTTTGGGTG TGGRATGTCR GCG

33

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGTAATGTG GGGGGGGAGG TTAAACCTCC CCC

33

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATAGATGYT GGGTCTTGGT TARGAARGAC TTG

33

30

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

- 39 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGACGGGCG GGATCTAACG GTATAACTGG CAG

33

(2) INFORMATION FOR SEQ ID NO:48:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATATTGGTC TCGGGGATCA GTATGCCTTT GTA

33

(2) INFORMATION FOR SEQ ID NO:49:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCACTAATGA TTGAACTTGA GAAGGATTTA AAT

33

(2) INFORMATION FOR SEQ ID NO:50:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

30 TCGGCGAGTT CTGTGACAGG GCCTGCCGCA GCT

33

(2) INFORMATION FOR SEQ ID NO:51:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-40-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCCTAGGAG GGGCAGGGTT TGGACTAGTC TAC

33

5 (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CAGTRGTGGT GCCAGTGAGG GTCAGCATAA TAG

33

(2) INFORMATION FOR SEQ ID NO:53:

- 15 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CAAGTGGCCA CTGCTSCTTG GACTGGAACA CYA

33

(2) INFORMATION FOR SEQ ID NO:54:

- 25 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AGGCATAGGA CCCGTGTCTT

20

(2) INFORMATION FOR SEQ ID NO:55:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

-41-

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
CTTCTTTGGA GAAAGTGGTG

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**Listings of All
Cycles, Procedures, and Sequences
Used to Synthesize the 15X Comb**

**Contained on the 3½" floppy disk
for the 380B DNA Synthesizer**

COMPLETE FILE DIRECTORY
VERSION 2.00

DISK NAME: 15X COMB
DATE: Aug 27, 1991
TIME: 13:50

FILE NAME	LAST ACCESS	DATE CREATED	FILE NAME	LAST ACCESS	DATE CREATED
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FILE TYPE: SYNTHESIS CYCLE

6.4XSC-5	08	27, 1991	08	27, 1991	6.4XS-5	08	27, 1991	08	27, 1991
1.2XD-6	08	27, 1991	08	27, 1991	1.2X-6	08	27, 1991	08	27, 1991
sscaaf3	01	07, 1990	01	07, 1990	caaf3	01	07, 1990	01	07, 1990
l0caaf3	01	07, 1990	01	07, 1990	haaf3	01	07, 1990	01	07, 1990
l0haaf3	01	07, 1990	01	07, 1990	rnaaf3	01	07, 1990	01	07, 1990
l0rnaaf3	01	07, 1990	01	07, 1990	sscaaf3	01	07, 1990	01	07, 1990
caaf3	01	07, 1990	01	07, 1990	l0caaf3	01	07, 1990	01	07, 1990
l0haaf3	01	07, 1990	01	07, 1990	rnaaf3	01	07, 1990	01	07, 1990
l0rnaaf3	01	07, 1990	01	07, 1990	sscaaf1	01	07, 1990	01	07, 1990
caaf1	01	07, 1990	01	07, 1990	l0caaf1	01	07, 1990	01	07, 1990
haaf1	01	07, 1990	01	07, 1990	l0haaf1	01	07, 1990	01	07, 1990
rnaaf1	01	07, 1990	01	07, 1990	l0rnaaf1	01	07, 1990	01	07, 1990
sscaaf1	01	07, 1990	01	07, 1990	caaf1	01	07, 1990	01	07, 1990
l0caaf1	01	07, 1990	01	07, 1990	l0haaf1	01	07, 1990	01	07, 1990
l0haaf1	01	07, 1990	01	07, 1990	l0rnaaf1	01	07, 1990	01	07, 1990
l0rnaaf1	01	07, 1990	01	07, 1990	caaf1	01	07, 1990	01	07, 1990
caaf1	01	07, 1990	01	07, 1990	l0haaf1	01	07, 1990	01	07, 1990
haaf1	01	07, 1990	01	07, 1990	l0rnaaf1	01	07, 1990	01	07, 1990

FILE TYPE: BOTTLE CHANGE PROCEDURE

bc 18	07	01, 1986	07	01, 1986	bc 17	07	01, 1986	07	01, 1986
bc 16	07	01, 1986	07	01, 1986	bc 15	07	01, 1986	07	01, 1986
bc 14	07	01, 1986	07	01, 1986	bc 13	07	01, 1986	07	01, 1986
bc 12	07	01, 1986	07	01, 1986	bc 11	07	01, 1986	07	01, 1986
bc 10	07	01, 1986	07	01, 1986	bc 9	07	01, 1986	07	01, 1986
bc 8a	07	01, 1986	07	01, 1986	bc 7	07	01, 1986	07	01, 1986
bc 6	07	01, 1986	07	01, 1986	bc 5	07	01, 1986	07	01, 1986
bc 4	07	01, 1986	07	01, 1986	bc 3	07	01, 1986	07	01, 1986
bc 2	07	01, 1986	07	01, 1986	bc 1	07	01, 1986	07	01, 1986

FILE TYPE: END PROCEDURE

CAP-PRIM	08	27, 1991	08	27, 1991	CE NH3	08	27, 1991	08	27, 1991
dearce	10	08, 1990	10	08, 1990	dearce10	10	08, 1990	10	08, 1990
dearho	10	08, 1990	10	08, 1990	dearho10	10	08, 1990	10	08, 1990
dearna	10	08, 1990	10	08, 1990	dearna10	10	08, 1990	10	08, 1990

FILE TYPE: BEGIN PROCEDURE

STD PREP	08	27, 1991	08	27, 1991	phos003	07	01, 1986	07	01, 1986
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FILE TYPE: SHUT-DOWN PROCEDURE

clean003	07	01, 1986	07	01, 1986
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FILE TYPE: DNA SEQUENCES

15X-2	08	27, 1991	08	27, 1991	15X-1	08	27, 1991	08	27, 1991
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SYNTHESIS CYCLE
VERSION 2.00

CYCLE NAME: 5.4XSC-5
NUMBER OF STEPS: 176
DATE: Aug 27, 199
TIME: 13:53

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	G	C	T	S	S	7	
1	10 #18 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
4	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	5 Advance FC	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	29 Phos Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
9	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
10	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
19	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
20	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
21	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
22	4 Wait	15	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
23	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
24	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
25	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
26	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
27	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
28	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
29	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
30	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
31	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
32	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
33	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
34	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
35	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
36	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
37	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
38	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
39	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
40	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
41	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
42	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
43	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.20CYCLE NAME: 5.4XSC-5
NUMBER OF STEPS: 175

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	G	C	T	S	S	7	
44	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
45	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
46	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
47	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
48	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
49	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
50	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
51	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
52	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
53	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
54	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
55	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
56	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
57	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
58	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
59	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
60	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
61	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
62	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
63	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
64	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
65	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
66	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
67	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
68	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
69	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
70	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
71	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
72	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
73	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
74	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
75	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
76	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
77	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
78	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
79	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
80	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
81	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
82	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
83	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
84	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
85	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
86	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
87	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
88	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.20

CYCLE NAME: 3.4XSC-5
NUMBER OF STEPS: 175

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	E	C	T	S	S	7	
99	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
90	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
91	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
92	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
93	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
94	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
95	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
96	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
97	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
98	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
99	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
100	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
101	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
102	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
103	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
104	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
105	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
106	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
107	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
108	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
109	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
110	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
111	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
112	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
113	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
114	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
115	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
116	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
117	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
118	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
119	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
120	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
121	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
122	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
123	-48 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
124	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
125	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
126	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
127	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
128	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
129	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
130	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
131	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
132	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
133	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.00

CYCLE NAME: 5.4XSC-S
NUMBER OF STEPS: 176

[illegible]

SYNTHESIS CYCLE
VERSION 2.20

CYCLE NAME: 5.4XS-5
 NUMBER OF STEPS: 132
 DATE: Aug 27, 199
 TIME: 13:56

STEP NUMBER	FUNCTION ± NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	S	S	7	
1	10 318 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	9 318 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
4	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	5 Advance FC	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	28 Phos Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
9	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
10	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
19	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
20	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
21	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
22	4 Wait	15	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
23	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
24	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
25	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
26	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
27	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
28	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
29	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
30	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
31	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
32	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
33	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
34	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
35	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
36	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
37	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
38	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
39	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
40	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
41	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
42	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
43	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.00CYCLE NAME: S.4XS-5
NUMBER OF STEPS: 32

STEP NUMBER	FUNCTION NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	G	C	T	S	S	7	
44	+47 Group 2 On	= 1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
45	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
46	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
47	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
48	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
49	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
50	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
51	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
52	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
53	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
54	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
55	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
56	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
57	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
58	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
59	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
60	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
61	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
62	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
63	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
64	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
65	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
66	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
67	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
68	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
69	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
70	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
71	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
72	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
73	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
74	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
75	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
76	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
77	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
78	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
79	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
80	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
81	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
82	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
83	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
84	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
85	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
86	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
87	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
88	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.00CYCLE NAME: 5.4XS-5
NUMBER OF STEPS: 132

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	S	S	7	
89	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
90	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
91	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
92	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
93	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
94	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
95	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
96	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
97	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
98	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
99	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
100	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
101	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
102	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
103	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
104	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
105	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
106	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
107	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
108	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
109	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
110	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
111	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
112	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
113	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
114	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
115	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
116	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
117	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
118	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
119	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
120	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
121	19 B+TET To Col 1	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
122	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
123	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
124	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
125	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
126	20 B+TET To Col 2	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
127	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
128	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
129	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
130	90 TET To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
131	21 B+TET To Col 3	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
132	90 TET To Column	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
133	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

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SYNTHESIS CYCLE
VERSION 2.00CYCLE NAME: 5.4XS-5
NUMBER OF STEPS: 132

STEP NUMBER	FUNCTION 3. NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	S	S	7	
134	4 Wait	50	Yes	Yes	Yes	Yes	Yes	Yes	Yes	
135	16 Cap Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
136	10 #18 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
137	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
138	1 Block Flush	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
139	91 Cap To Column	22	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
140	10 #18 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
141	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
142	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
143	1 Block Flush	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
144	81 #15 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
145	13 #15 To Column	22	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
146	10 #18 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
147	4 Wait	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
148	2 Reverse Flush	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
149	1 Block Flush	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
150	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
151	34 Flush to Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
152	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
153	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
154	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
155	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
156	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
157	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
158	1 Block Flush	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
159	33 Cycle Entry	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
160	6 Waste-Port	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
161	37 Relay 3 Pulse	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
162	82 #14 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
163	30 #17 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
164	10 #18 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
165	9 #18 To Column	20	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
166	11 #17 To Column	60	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
167	14 #14 To Column	20	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
168	2 Reverse Flush	7	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
169	11 #17 To Column	15	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
170	34 Flush to Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
171	11 #17 To Column	15	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
172	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
173	14 #14 To Column	20	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
174	34 Flush to Waste	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
175	7 Waste-Bottle	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
176	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
177	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
178	9 #18 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

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SYNTHESIS CYCLE
VERSION 2.00

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CYCLE NAME: 5.4XS-5
NUMBER OF STEPS: 132

[illegible]

SYNTHESIS CYCLE
VERSION 2.00

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CYCLE NAME: 1.2X0-6
 NUMBER OF STEPS: 120
 DATE: Aug 27, 199
 TIME: 14:00

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	G	C	T	E	S	7	
1	10 \$18 To Waste	2	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	9 \$18 To Column	9	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
4	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	5 Advance FC	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	28 Phos Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
9	19 B+TET To Col 1	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
10	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	19 B+TET To Col 1	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	19 B+TET To Col 1	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	10 \$18 To Waste	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
19	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
20	20 B+TET To Col 2	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
21	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
22	20 B+TET To Col 2	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
23	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
24	20 B+TET To Col 2	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
25	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
26	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
27	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
28	10 \$18 To Waste	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
29	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
30	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
31	21 B+TET To Col 3	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
32	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
33	21 B+TET To Col 3	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
34	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
35	21 B+TET To Col 3	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
36	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
37	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
38	4 Wait	20	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
39	2 Reverse Flush	5					Yes			Yes
40	10 \$18 To Waste	2					Yes			Yes
41	9 \$18 To Column	9					Yes			Yes
42	2 Reverse Flush	5					Yes			Yes
43	10 \$18 To Waste	3					Yes			Yes

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SYNTHESIS CYCLE
VERSION 2.00

CYCLE NAME: 1.2XD-S
NUMBER OF STEPS: 120

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	S	6	7	
44	1 Block Flush	- 3					Yes			Yes
45	+45 Group 1 On	1					Yes			Yes
46	90 TET To Column	6					Yes			Yes
47	19 B+TET To Col 1	6					Yes			Yes
48	90 TET To Column	3					Yes			Yes
49	19 B+TET To Col 1	3					Yes			Yes
50	90 TET To Column	3					Yes			Yes
51	19 B+TET To Col 1	3					Yes			Yes
52	9 \$18 To Column	1					Yes			Yes
53	-46 Group 1 Off	1					Yes			Yes
54	+47 Group 2 On	1					Yes			Yes
55	10 \$18 To Waste	4					Yes			Yes
56	1 Block Flush	3					Yes			Yes
57	90 TET To Column	6					Yes			Yes
58	20 B+TET To Col 2	6					Yes			Yes
59	90 TET To Column	3					Yes			Yes
60	20 B+TET To Col 2	3					Yes			Yes
61	90 TET To Column	3					Yes			Yes
62	20 B+TET To Col 2	3					Yes			Yes
63	9 \$18 To Column	1					Yes			Yes
64	-48 Group 2 Off	1					Yes			Yes
65	+49 Group 3 On	1					Yes			Yes
66	10 \$18 To Waste	4					Yes			Yes
67	1 Block Flush	3					Yes			Yes
68	90 TET To Column	6					Yes			Yes
69	21 B+TET To Col 3	6					Yes			Yes
70	90 TET To Column	3					Yes			Yes
71	21 B+TET To Col 3	3					Yes			Yes
72	90 TET To Column	3					Yes			Yes
73	21 B+TET To Col 3	3					Yes			Yes
74	9 \$18 To Column	1					Yes			Yes
75	-50 Group 3 Off	1					Yes			Yes
76	4 Wait	20					Yes			Yes
77	16 Cap Pres	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
78	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
79	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
80	91 Cap To Column	12	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
81	10 \$18 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
82	4 Wait	8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
83	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
84	81 \$15 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
85	13 \$15 To Column	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
86	10 \$18 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
87	4 Wait	15	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
88	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

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SYNTHESIS CYCLE
VERSION 2.00

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CYCLE NAME: 1.2X0-6
NUMBER OF STEPS: 120

<u>STEP</u>	<u>FUNCTION</u>	<u>STEP</u>	<u>STEP ACTIVE FOR BASES</u>	<u>SAFE</u>
<u>NUMBER</u>	<u># NAME</u>	<u>TIME</u>	A B C T S 6 7	<u>STEP</u>
89	9 \$18 To Column	- 9	Yes Yes Yes Yes Yes Yes Yes	Yes
90	34 Flush to Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
91	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
92	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
93	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
94	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
95	1 Block Flush	3	Yes Yes Yes Yes Yes Yes Yes	Yes
96	33 Cycle Entry	1	Yes Yes Yes Yes Yes Yes Yes	Yes
97	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
98	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
99	6 Waste-Port	1	Yes Yes Yes Yes Yes Yes Yes	Yes
100	30 \$17 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
101	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
102	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
103	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
104	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
105	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
106	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
107	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
108	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
109	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
110	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
111	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
112	34 Flush to Waste	5	Yes Yes Yes Yes Yes Yes Yes	No
113	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	No
114	34 Flush to Waste	7	Yes Yes Yes Yes Yes Yes Yes	No
115	7 Waste-Bottle	1	Yes Yes Yes Yes Yes Yes Yes	Yes
116	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
117	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
118	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
119	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
120	1 Block Flush.	3	Yes Yes Yes Yes Yes Yes Yes	Yes

SYNTHESIS CYCLE
VERSION 2.20

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CYCLE NAME: 1.2X-3
 NUMBER OF STEPS: 32
 DATE: Aug 27, 199
 TIME: 14:02

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	5	6	7	
1	10 \$18 To Waste	2	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	9 \$18 To Column	9	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
4	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	5 Advance FC	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	28 Phos Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	+45 Group 1 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
9	19 B+TET To Col 1	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
10	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	19 B+TET To Col 1	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	19 B+TET To Col 1	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	-46 Group 1 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	+47 Group 2 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	10 \$18 To Waste	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
19	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
20	20 B+TET To Col 2	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
21	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
22	20 B+TET To Col 2	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
23	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
24	20 B+TET To Col 2	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
25	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
26	-48 Group 2 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
27	+49 Group 3 On	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
28	10 \$18 To Waste	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
29	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
30	90 TET To Column	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
31	21 B+TET To Col 3	6	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
32	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
33	21 B+TET To Col 3	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
34	90 TET To Column	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
35	21 B+TET To Col 3	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
36	9 \$18 To Column	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
37	-50 Group 3 Off	1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
38	4 Wait	20	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
39	16 Cap Prep	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
40	2 Reverse Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
41	1 Block Flush	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
42	91 Cap To Column	12	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
43	10 \$18 To Waste	3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

(Continued next page.)

SYNTHESIS CYCLE
VERSION 2.30

- 158 -

CYCLE NAME: 1.2X-5
NUMBER OF STEPS: 32

<u>STEP</u>	<u>FUNCTION</u>	<u>STEP</u>	<u>ACTIVE FOR BASES</u>	<u>SAFE</u>
<u>NUMBER</u>	<u>NAME</u>	<u>TIME</u>	A C T S E 7	<u>STEP</u>
44	4 Wait	= 8	Yes Yes Yes Yes Yes Yes Yes	Yes
45	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
46	31 \$15 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
47	13 \$15 To Column	10	Yes Yes Yes Yes Yes Yes Yes	Yes
48	10 \$18 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
49	4 Wait	15	Yes Yes Yes Yes Yes Yes Yes	Yes
50	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
51	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
52	34 Flush to Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
53	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
54	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
55	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
56	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
57	1 Block Flush	3	Yes Yes Yes Yes Yes Yes Yes	Yes
58	33 Cycle Entry	1	Yes Yes Yes Yes Yes Yes Yes	Yes
59	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
60	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
61	6 Waste-Port	1	Yes Yes Yes Yes Yes Yes Yes	Yes
62	30 \$17 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	No
63	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
64	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
65	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
66	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
67	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
68	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
69	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
70	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
71	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
72	34 Flush to Waste	1	Yes Yes Yes Yes Yes Yes Yes	No
73	11 \$17 To Column	7	Yes Yes Yes Yes Yes Yes Yes	No
74	34 Flush to Waste	5	Yes Yes Yes Yes Yes Yes Yes	No
75	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	No
76	34 Flush to Waste	7	Yes Yes Yes Yes Yes Yes Yes	No
77	7 Waste-Bottle	1	Yes Yes Yes Yes Yes Yes Yes	Yes
78	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
79	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
80	9 \$18 To Column	9	Yes Yes Yes Yes Yes Yes Yes	Yes
81	2 Reverse Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes
82	1 Block Flush	3	Yes Yes Yes Yes Yes Yes Yes	Yes

END PROCEDURE
VERSION 2.20

Page 1

PROCEDURE NAME: CAP-PRIM
NUMBER OF STEPS: 37
DATE: Aug 27, 199
TIME: 14:03

<u>STEP</u>	<u>FUNCTION</u>	<u>STEP</u>	<u>STEP ACTIVE FOR BASES</u>	<u>SAFE</u>
<u>NUMBER</u>	<u># NAME</u>	<u>TIME</u>	<u>A G C T S S 7</u>	<u>STEP</u>
1	10 \$18 To Waste	2	Yes Yes Yes Yes Yes Yes Yes	Yes
2	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
3	2 Reverse Flush	20	Yes Yes Yes Yes Yes Yes Yes	Yes
4	1 Block Flush	4	Yes Yes Yes Yes Yes Yes Yes	Yes
5	16 Cap Prep	10	Yes Yes Yes Yes Yes Yes Yes	Yes
6	91 Cap To Column	30	Yes Yes Yes Yes Yes Yes Yes	Yes
7	10 \$18 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
8	1 Block Flush	4	Yes Yes Yes Yes Yes Yes Yes	Yes
9	4 Wait	300	Yes Yes Yes Yes Yes Yes Yes	Yes
10	16 Cap Prep	10	Yes Yes Yes Yes Yes Yes Yes	Yes
11	91 Cap To Column	30	Yes Yes Yes Yes Yes Yes Yes	Yes
12	10 \$18 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
13	1 Block Flush	4	Yes Yes Yes Yes Yes Yes Yes	Yes
14	4 Wait	300	Yes Yes Yes Yes Yes Yes Yes	Yes
15	2 Reverse Flush	10	Yes Yes Yes Yes Yes Yes Yes	Yes
16	10 \$18 To Waste	3	Yes Yes Yes Yes Yes Yes Yes	Yes
17	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
18	2 Reverse Flush	10	Yes Yes Yes Yes Yes Yes Yes	Yes
19	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
20	2 Reverse Flush	10	Yes Yes Yes Yes Yes Yes Yes	Yes
21	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
22	2 Reverse Flush	10	Yes Yes Yes Yes Yes Yes Yes	Yes
23	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
24	2 Reverse Flush	10	Yes Yes Yes Yes Yes Yes Yes	Yes
25	9 \$18 To Column	15	Yes Yes Yes Yes Yes Yes Yes	Yes
26	2 Reverse Flush	60	Yes Yes Yes Yes Yes Yes Yes	Yes
27	1 Block Flush	5	Yes Yes Yes Yes Yes Yes Yes	Yes

END PROCEDURE
VERSION 2.20

Page 1

PROCEDURE NAME: 03 NHS
 NUMBER OF STEPS: 27
 DATE: Aug 27, 199
 TIME: 14:04

STEP NUMBER	FUNCTION # NAME	STEP TIME	STEP ACTIVE FOR BASES							SAFE STEP
			A	S	C	T	S	S	7	
1	2 Reverse Flush	60	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	27 310 To Collect	17	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	10 318 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
4	1 Block Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
5	4 Wait	660	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
6	27 310 To Collect	18	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	10 318 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	1 Block Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
9	4 Wait	660	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
10	27 310 To Collect	18	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	10 318 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	1 Block Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13	4 Wait	660	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	27 310 To Collect	17	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	10 318 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
16	1 Block Flush	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
17	4 Wait	660	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
18	8 Flush To CLCT	9	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
19	27 310 To Collect	14	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
20	8 Flush To CLCT	9	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
21	2 Reverse Flush	60	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
22	1 Block Flush	4	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
23	10 318 To Waste	5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
24	9 318 To Column	30	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
25	2 Reverse Flush	60	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
26	1 Block Flush	10	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
27	42 310 Vent	2	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

deprotection
 should not connect to NHS

**BEGIN PROCEDURE
VERSION 2.20**

350.

PROCEDURE NAME: STD PREP
NUMBER OF STEPS: 13
DATE: Aug 27, 199
TIME: 14:05

<u>STEP</u>	<u>FUNCTION</u>	<u>STEP</u>	<u>STEP ACTIVE FOR BASES</u>	<u>SAFE</u>
<u>NUMBER</u>	<u># NAME</u>	<u>TIME</u>	<u>A S C T E S 7</u>	<u>STEP</u>
1	28 Phos Prep	10	Yes Yes Yes Yes Yes Yes Yes	Yes
2	52 A To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
3	53 B To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
4	54 C To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
5	55 T To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
6	56 #5 To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
7	57 #6 To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
8	58 #7 To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
9	61 TET To Waste	8	Yes Yes Yes Yes Yes Yes Yes	Yes
10	10 #18 To Waste	10	Yes Yes Yes Yes Yes Yes Yes	Yes
11	16 Cap Prep	10	Yes Yes Yes Yes Yes Yes Yes	Yes
12	53 Cap A To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
13	60 Cap B To Waste	5	Yes Yes Yes Yes Yes Yes Yes	Yes
14	81 #15 To Waste	8	Yes Yes Yes Yes Yes Yes Yes	Yes
15	82 #14 To Waste	8	Yes Yes Yes Yes Yes Yes Yes	Yes
16	30 #17 To Waste	10	Yes Yes Yes Yes Yes Yes Yes	Yes
17	10 #18 To Waste	15	Yes Yes Yes Yes Yes Yes Yes	Yes
18	1 Block Flush	15	Yes Yes Yes Yes Yes Yes Yes	Yes

DNA SEQUENCE
VERSION 2.00

SEQUENCE NAME: 15X-1
SEQUENCE LENGTH: 71
DATE: Aug 27, 199
TIME: 14:07
COMMENT:

5'- GGT GTT TGG TTG TTS TTS TTS TTS TTS TTS TTS TTS

TTG TTG TTG TTG TTT TTT TTT TTT TTT TTT TT -3'

DNA SEQUENCE
VERSION 2.00

SEQUENCE NAME: 15X-2
SEQUENCE LENGTH: 10
DATE: Aug 27, 199
TIME: 14:06
COMMENT:

5'- TTT GAC TGG T -3'

Claims

1. A synthetic oligonucleotide useful as an
amplifier probe in a sandwich hybridization assay for
5 HTLV-1, wherein said oligonucleotide comprises:
a first segment comprising a nucleotide
sequence substantially complementary to a segment of
HTLV-1 nucleic acid; and
a second segment comprising a nucleotide
10 sequence substantially complementary to an
oligonucleotide unit of a nucleic acid multimer,
wherein said HTLV-1 nucleic acid segment is
selected from the group consisting of

- 15 GGTCTGGGTGTCAAYCTGGGCTTTAATTACGGG (SEQ ID NO:6),
ATCTAGTARAGCTTCGATAGTCTTTGGGTGGCT (SEQ ID NO:7),
GGCTATCGGAAGGACTGTCATGTCTGCTCCTGT (SEQ ID NO:8),
TGTRTTTTTGAGGGGAGTATTACTTGAGAACAA (SEQ ID NO:9),
ATCTTGGGTTTGGCCCCCTGCCCTAAYACGGA (SEQ ID NO:10),
20 TATTAGCACAGGAAGGGAGGTGAGCTTAAAGTG (SEQ ID NO:11),
TAAAACAATAGGCGTYGTCCGGAAGGGAGGCG (SEQ ID NO:12),
CYAGTTGTTTTTGGTATCAACTAGGCAAGATGT (SEQ ID NO:13),
GCATTGTTGTAAGGCATCRGACCTATGATGGC (SEQ ID NO:14),
CCYTTTTGCCTCAGGGAGGTACAGGACGCCYTG (SEQ ID NO:15),
25 RGCTGGCGCCTGTATTGGCAAGATTACAGGCGG (SEQ ID NO:16),
GGGGGGCCTTGGGAGGTGTTCTAGYCCAAGGAC (SEQ ID NO:17),
GGCGTTCTGGTTTAAAGGGAAGTGGCTGATTTT (SEQ ID NO:18),
GGGCCTTCCGGACCAAGTGTGCAAGGCCTGGA (SEQ ID NO:19),
GCCCGGTGTAGGRTTCGATATGGCCTGCCTCCA (SEQ ID NO:20),
30 CYTTTTTAACTGGGAATACTGGGTTATTTCCTG (SEQ ID NO:21),
GCAGGTCGTGGATGAATCGCCAGGTTCCATTGG (SEQ ID NO:22),
ATGAGAGRTCTATGGTTAGAGAGTTAGTGGCCC (SEQ ID NO:23),
GGCTGGACAAGTCAGGGGGCCCGGGGAAGATG (SEQ ID NO:24),
CTATAGTTTGYAAGTGGGCTAGTGTGTTGGCA (SEQ ID NO:25),
35 GTARGGGGATTGGAAGGCGTCTYTAAGGT (SEQ ID NO:26),

5 CAGTGAAAGCAAAGTAGGGCTGGAAGTGTTTAG (SEQ ID NO:27),
TAGTGCCGGGGCCGTAGTTACACTGCTGTGGGA (SEQ ID NO:28),
TAAACCCTTGGGGTAGTACTYTCAGGCGTATC (SEQ ID NO:29),
CCAGCTGCATTTTCGAACAGGGTGGGACTATTTT (SEQ ID NO:30),
GGAARGCTTGCCGAATGGGCTGCAGGATATGGG (SEQ ID NO:31),
TGTCATCCATGTACTGAAGAATAGTGCATTGGG (SEQ ID NO:32),
GYAGGTCCCKCATGGGAGGGGCTTGCTYAGGAGAA (SEQ ID NO:33),
TTAGGGAAGCCATTGTGGCCTCTGAGAGTAGTW (SEQ ID NO:34),
10 TTTTGTTPPTCGGACACAGGCAACCCATGGGAGA (SEQ ID NO:35),
CTAGGAACTTAATTGTTCCAGGGGTTTGCTGGG (SEQ ID NO:36),
CATAAGTCAGGTGATTTRGGTGAAATTATYTGCC (SEQ ID NO:37),
AGCGGGACCGTATAGGTACCKTGGGGACTGCAT (SEQ ID NO:38),
CGCCAAGTAGGGCTTGAAGTTCAGGTAGCGCCC (SEQ ID NO:39),
AGGTAGGAGTTCCTTTGGAGACCCACTGAATCT (SEQ ID NO:40),
15 AGGCACAGTAGAGACTGTGAAGGGGCTGGCGTA (SEQ ID NO:41).

2. The synthetic oligonucleotide of claim 1,
wherein said second segment comprises the sequence
AGGCATAGGACCCGTGTCTT (SEQ ID NO:54).

3. A synthetic oligonucleotide useful as a
capture probe in a sandwich hybridization assay for HTLV-
1, wherein the synthetic oligonucleotide comprises:

25 a first segment comprising a nucleotide
sequence substantially complementary to a segment of
HTLV-1 nucleic acid; and

a second segment comprising a nucleotide
sequence substantially complementary to an
oligonucleotide bound to a solid phase,

30 wherein said HTLV-1 nucleic acid segment is
selected from the group consisting of

35 TCTGGTTCTGGGATAGTGGGCTTTAGGCGGGGG (SEQ ID NO:42),
GGGAGRTCTAATAGGAGGGCATCYTCCTCTGGC (SEQ ID NO:43),
CCTATGRAGTTTTTTGGGTGTGGRATGTCRGGC (SEQ ID NO:44),
CTGTAATGTGGGGGGGGAGGTTAAACCTCCCCC (SEQ ID NO:45),

5 AATAGATGYTGGGTCTTGGTTARGAARGACTTG (SEQ ID NO:46),
CCGACGGGCGGGATCTAACGGTATAACTGGCAG (SEQ ID NO:47),
ATATTGGTCTCGGGGATCAGTATGCCTTTGTA (SEQ ID NO:48),
GCACTAATGATTGAACTTGAGAAGGATTTAAAT (SEQ ID NO:49),
TGCGGCAGTTCTGTGACAGGGCCTGCCGCAGCT (SEQ ID NO:50),
CCCCTAGGAGGGGCAGGGTTTGGACTAGTCTAC (SEQ ID NO:51),
CAGTRGTGGTGCCAGTGAGGGTCAGCATAATAG (SEQ ID NO:52),
CAAGTGGCCACTGCTSCCTGGACTGGAACACYA (SEQ ID NO:53).

10 4. The synthetic oligonucleotide of claim 3,
wherein said second segment comprises

CTTCTTTGGAGAAAGTGGTG (SEQ ID NO:55).

15 5. A set of synthetic oligonucleotides useful
as amplifier probes in a sandwich hybridization assay for
HTLV-1, comprising two oligonucleotides,
wherein each oligonucleotide comprises:
a first segment comprising a nucleotide
20 sequence substantially complementary to a segment of
HTLV-1 nucleic acid; and
a second segment comprising a nucleotide
sequence substantially complementary to an
oligonucleotide unit of a nucleic acid multimer,
25 wherein said HTLV-1 nucleic acid segments are

30 GGTCTGGGTGTCAAYCTGGGCTTTAATTACGGG (SEQ ID NO:6),
ATCTAGTARAGCTTCGATAGTCTTTGGGTGGCT (SEQ ID NO:7),
GGCTATCGGAAGGACTGTCTGTCTCCTGT (SEQ ID NO:8),
TGTRTTTTTGAGGGGAGTATTACTTGAGAACAA (SEQ ID NO:9),
ATCTTGGGTTTGGCCCCCTGCCCCCTAAYACGGA (SEQ ID NO:10),
TATTAGCACAGGAAGGGAGGTGAGCTTAAAGTG (SEQ ID NO:11),
TAAACAATAGGCGTYGTCCGGAAAGGGAGGCG (SEQ ID NO:12),
CYAGTTGTTTTTGGTATCAACTAGGCAAGATGT (SEQ ID NO:13),
35 GCATTGTTGTAAGGCATCRGACCTATGATGGC (SEQ ID NO:14),

CCYTTTTGCCTCAGGGAGGTACAGGACGCCYTG (SEQ ID NO:15),
RGCTGGCGCCTGTATTGGCAAGATTACAGGCGG (SEQ ID NO:16),
GGGGGGCCTTGGGAGGTGTTCTAGYCCAAGGAC (SEQ ID NO:17),
GGCGTTCTGGTTTAAAGGGAAGTGGCTGATTTT (SEQ ID NO:18),
5 GGGCCTTCCGGACCAAGTGTTGCAAGGCCTGGA (SEQ ID NO:19),
GCCCCGGTGTAGGRITTCGATATGGCCTGCCTCCA (SEQ ID NO:20),
CYTTTTTAACTGGGAATACTGGGTTATTYCCTG (SEQ ID NO:21),
GCAGGTGCTGGATGAATCGCCAGGTTCCATTGG (SEQ ID NO:22),
ATGAGAGRTCTATGGTTAGAGAGTTAGTGGCCC (SEQ ID NO:23),
10 GGCTGGACAAGTCAGGGGGCCCGGGGAAGATG (SEQ ID NO:24),
CTATAGTTTGAAAGTGGGCTAGTGTRGTTGGCA (SEQ ID NO:25),
GTARGGGGATTTGGAAAAGGCGTCTYTAAGGT (SEQ ID NO:26),
CAGTGAAAGCAAAGTAGGGCTGGAAGTGTTCAG (SEQ ID NO:27),
TAGTGCCGGGGCCGTAGTTACACTGCTGTGGGA (SEQ ID NO:28),
15 TAAACCCTTGGGGTAGTACTYTCAGGCGTATC (SEQ ID NO:29),
CCAGCTGCATTTGGAACAGGGTGGGACTATTTT (SEQ ID NO:30),
GGAARGCTTGCCGAATGGGCTGCAGGATATGGG (SEQ ID NO:31),
TGTCATCCATGTACTGAAGAATAGTGCATTGGG (SEQ ID NO:32),
GYAGGTCCCATGGGAGGGGCTTGCTYAGGAGAA (SEQ ID NO:33),
20 TTAGGGAAGCCATTGTGGCCTCTGAGAGTAGTW (SEQ ID NO:34),
TTTGTGTTTTCGGACACAGGCAACCCATGGGAGA (SEQ ID NO:35),
CTAGGAACTTAATTGTTCCAGGGGTTTGCTGGG (SEQ ID NO:36),
CATAAGTGAGGTGATTTRGGTGAAATTATYTGCC (SEQ ID NO:37),
AGCGGGACCGTATAGGTACCKTGGGGACTGCAT (SEQ ID NO:38),
25 CGCCAAGTAGGGCTTGAAGTTCAGGTAGCGCCC (SEQ ID NO:39),
AGGTAGGAGTTCCTTTGGAGACCCACTGAATCT (SEQ ID NO:40),
AGGCACAGTAGAGACTGTGAAGGGGCTGGCGTA (SEQ ID NO:41).

6. The synthetic oligonucleotide of claim 5,
30 wherein said second segment comprises
AGGCATAGGACCCGTGTCTT (SEQ ID NO:54).

7. A set of synthetic oligonucleotides useful
as capture probes in a sandwich hybridization assay for
35 HTLV-1, comprising two oligonucleotides,

wherein each oligonucleotide comprises:
a first segment comprising a nucleotide
sequence substantially complementary to a segment of
HTLV-1 nucleic acid; and

5 a second segment comprising a nucleotide
sequence substantially complementary to an
oligonucleotide bound to a solid phase,

wherein said HTLV-1 nucleic acid segments are

10 TCTGGTTCTGGGATAGTGGGCTTTAGGCGGGGG (SEQ ID NO:42),
GGGAGRTCTAATAGGAGGGCATCYTCCTCTGGC (SEQ ID NO:43),
CCTATGRAGTTTTTTGGGTGTGGRATGTCRGCG (SEQ ID NO:44),
CTGTAATGTGGGGGGGAGGTTAAACCTCCCCC (SEQ ID NO:45),
AATAGATGYTGGGTCTTGGTTARGAARGACTTG (SEQ ID NO:46),
15 CCGACGGGCGGGATCTAACGGTATAACTGGCAG (SEQ ID NO:47),
ATATTTGGTCTCGGGGATCAGTATGCCTTTGTA (SEQ ID NO:48),
GCACTAATGATTGAACCTTGAGAAGGATTTAAAT (SEQ ID NO:49),
TGCGGCAGTTCTGTGACAGGGCCTGCCGCAGCT (SEQ ID NO:50),
CCCCTAGGAGGGGCAGGGTTTGGACTAGTCTAC (SEQ ID NO:51),
20 CAGTRGTGGTGCCAGTGAGGGTCAGCATAATAG (SEQ ID NO:52),
CAAGTGGCCACTGCTSCCTGGACTGGAACACYA (SEQ ID NO:53).

8. The synthetic oligonucleotide of claim 7,
wherein said second segment comprises

25 CTTCTTTGGAGAAAGTGGTG (SEQ ID NO:55).

9. A solution sandwich hybridization assay
for detecting the presence of HTLV-1 in a sample,
30 comprising

(a) contacting the sample under hybridizing
conditions with an excess of (i) amplifier probes
comprising the set of synthetic oligonucleotides of claim
5 and (ii) a set of capture probe oligonucleotides
35 wherein the capture probe oligonucleotide comprises a

first segment comprising a nucleotide sequence that is substantially complementary to a segment of HTLV-1 nucleic acid and a second segment that is substantially complementary to an oligonucleotide bound to a solid phase;

(b) contacting the product of step (a) under hybridizing conditions with said oligonucleotide bound to the solid phase;

(c) thereafter separating materials not bound to the solid phase;

(d) contacting the bound product of step (c) under hybridization conditions with the nucleic acid multimer, said multimer comprising at least one oligonucleotide unit that is substantially complementary to the second segment of the amplifier probe polynucleotide and a multiplicity of second oligonucleotide units that are substantially complementary to a labeled oligonucleotide;

(e) removing unbound multimer;

(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;

(g) removing unbound labeled oligonucleotide; and

(h) detecting the presence of label in the solid phase complex product of step (g).

10. A solution sandwich hybridization assay for detecting the presence of HTLV-1 in a sample, comprising

(a) contacting the sample under hybridizing conditions with an excess of (i) a set of amplifier probe oligonucleotides wherein the amplifier probe oligonucleotide comprises a first segment comprising a nucleotide sequence substantially complementary to a

segment of HTLV-1 nucleic acid and a second segment comprising a nucleotide sequence substantially complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) capture probes comprising the set
5 of synthetic oligonucleotides of claim 7;

(b) contacting the product of step (a) under hybridizing conditions with said oligonucleotide bound to the solid phase;

(c) thereafter separating materials not bound
10 to the solid phase;

(d) contacting the bound product of step (c) under hybridization conditions with the nucleic acid multimer, said multimer comprising at least one oligonucleotide unit that is substantially complementary
15 to the second segment of the amplifier probe polynucleotide and a multiplicity of second oligonucleotide units that are substantially complementary to a labeled oligonucleotide;

(e) removing unbound multimer;

(f) contacting under hybridizing conditions the
20 solid phase complex product of step (e) with the labeled oligonucleotide;

(g) removing unbound labeled oligonucleotide;
and

(h) detecting the presence of label in the
25 solid phase complex product of step (g).

11. A kit for the detection of HTLV-1 in a sample comprising in combination

(i) a set of amplifier probe oligonucleotides
30 wherein the amplifier probe oligonucleotide comprises a first segment comprising a nucleotide sequence substantially complementary to a segment of HTLV-1 nucleic acid and a second segment comprising a nucleotide
35

sequence substantially complementary to an
oligonucleotide unit of a nucleic acid multimer;

(ii) a set of capture probe oligonucleotides
wherein the capture probe oligonucleotide comprises a
5 first segment comprising a nucleotide sequence that is
substantially complementary to a segment of HTLV-1
nucleic acid and a second segment that is substantially
complementary to an oligonucleotide bound to a solid
phase;

10 (iii) a nucleic acid multimer, said multimer
comprising at least one oligonucleotide unit that is
substantially complementary to the second segment of the
amplifier probe polynucleotide and a multiplicity of
second oligonucleotide units that are substantially
15 complementary to a labeled oligonucleotide; and
(iv) a labeled oligonucleotide.

12. The kit of claim 11, further comprising
instructions for the use thereof.

20

13. The kit of claim 11, wherein said set of
amplifier probe oligonucleotides is the set of synthetic
oligonucleotides of claim 5.

25 14. The kit of claim 11, wherein said set of
capture probe oligonucleotides is the set of synthetic
oligonucleotides of claim 7.

30

35

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/11345

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : C12Q 1/68; C07H 21/04

US CL : 435/6; 536/24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Medline, APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	Proc. Natl. Acad. Sci., Vo. 80, issued 1983, Seiki et al., "Human adult T-cell leukemia virus: Complete nucleotide sequence of the provirus genome integrated in leukemia cell DNA," pages 3618-3622. See sequence search results.	<u>1,3,5,7</u> 2,4,6,8,9-14
Y	WO, A, 8903891 (Urdea et al.) 05 May 1989, see abstract.	2,4,6,8,9-14
Y	EP, A, 0139489 (Peter) 02 May 1985, see entire document.	2,4,6,8,9-14

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be part of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

08 February 1993

Date of mailing of the international search report

9 MAR 1993

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